

```

seq_name: gb_dal:ECFABHDG
seq_documentation_block:
  LOCUS       ECFABHDG             1440 bp            DNA                    BCT              30-JUN-1993
  DEFINITION   E.coli fabH and fabD genes for 2-ketoacyl-acyl carrier protein synthase III and malonyl CoA-acyl carrier protein transacylase.
  ACCESSION   Z11565.1
  VERSION     Z11565.1 GI:41363
  KEYWORDS    2-ketoacyl-acyl carrier protein synthase III; malonyl CoA-acyl carrier protein transacylase.
  SOURCE      Escherichia coli.
  ORGANISM    Escherichia coli.
               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
  REFERENCE   1 (bases 1 to 1440)
               Magnuson,K., Oh,W., Larson,T.J. and Cronan,J.E. Jr. Cloning and nucleotide sequence of the fabD gene encoding malonyl Coenzyme A-acyl carrier protein transacylase of Escherichia coli PBBS Lett. 299 (3), 262-266 (1992)
  JOURNAL     92183950
  MEDLINE     2 (bases 1 to 479)
  REFERENCE   Tsay,J., Oh,W., Larson,T.J., Jackowski,S. and Rock,C.O. Isolation and characterization of the 2-ketoacyl-acyl carrier protein synthase III gene (fabH) from Escherichia coli K-12 5. Biol. Chem. (1992) In press
  AUTHORS     3 (bases 1 to 1440)
  TITLE       Larson,T.
  JOURNAL     Direct Submission
  REFERENCE   Submitted (09-JAN-1992) Larson T., Virginia Polytechnic Institute and State University, Blacksburg, Virginia, USA
  FEATURES
  source
    1..1440
    /organism="Escherichia coli"
    /strain="K12"
    /db_xref="taxon:562"
    1..355
    /gene="fabH"
    <1..355
    /gene="fabH"
    /citation=[1]
    /citation=[2]
    /codon_start=2
    /transl_table=11
    /evidence=experimental
    /product="2-ketoacyl-acyl carrier protein synthase III"
    /protein_id="CAA77659.1"
    /db_xref="GI:41365"
    /db_xref="SWISS-PROT:P24249"
    /translation="NSHLTMAGNEVFKVAVELAHIVDETLAANNLRSLDWLVPFQALRLRTISAATKLGMNDNVVYTLDRHNTSAAVSVPALDEAVRNGIKRGQVLLEAFEGGTWSSALVRF"
    360..363
    /gene="fabD"
    /standard_name="ribosome binding site"
    /citation=[1]
    /citation=[2]
    /evidence=experimental
    360..1300
    /gene="fabD"
    371..1300
    /gene="fabD"
    /citation=[1]
    /citation=[2]
    /codon_start=1
    /transl_table=11
    /product="malonyl CoA-acyl carrier protein transacylase"
    /protein_id="CAA77658.1"
    /db_xref="GI:41364"
    /db_xref="SWISS-PROT:P25715"
    /translation="MTOFAFVPCGSGOTVGLADMAASYPIVETFAFSAALGVDLWALDQGEELNKTQOTOPALITASALVATRWVOCGRAPMAKSHSGEYSATLCAWIFPADVRLVLEIRGKFMQEAVIDEGGMAAIIIGLDDSIARACEEAAGOVSPVN FNSGQVVIADHKAVERBAGACCAAGAKALDLPVSPVSHCALMKPADKLAIVELAK

```

ITPNAPIPVVNNNDVKCTNGDAIRDALVROLINPVQWTKSVFYMAAGVEHLYEVG  
 BASE COUNT 332 a 347 c 440 g 321 t  
 ORIGIN

alignment\_scores:  
 Quality: 643.50 Length: 310  
 Ratio: 2.786 Gaps: 4  
 Percent Similarity: 74.516 Percent Identity: 45.484

alignment\_block:

us-09-308-397-2 x ECFABHDG ..

Align seg 1/1 to: ECFABHDG from: 1 to: 1440

```

1 MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuG1 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
371 ATGACCAATTCATTCATTTGTTCCCTGAGCAGGGTTCTCAACCGTTGG 420
17 yMetGlyArgAspPheTyrAspGlnTyrProIleValIleGlnTyrIleA 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
421 AATGCTGCTGATATGCGCGAGCTATCCATGTGCGAAGAAAGCTTGG 470
34 sParGAlaSerGlnValLeuGlyTyrAspLeuArgTyrLeuIleAspThr 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
471 CTGAACCTTCTGCGGCTGAGCTACGACCTGCGGCGCTG.....ACC 514
51 GUGLU.....AspLysLeuAsnGlnThrArgTyrTyrGlnProAl 64
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
515 CAGCAGGGCGCAGCTGAACACTGAATTAACCTGCAACCTACCGCTGC 564
64 aIleLeuAlaThrSerValAlaIleTyrArgLeuGlnGlnTyrGlyT 81
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
565 GCGTTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 614
81 yGln...ProAspMetValAlaGlyLeuSerLeuGlnTyrSerAla 96
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
615 GTAAGCACCAGCAATGATGCGGCTGACACGCTGGGGAAATACCTCCG 664
97 LeuValAlaSerGlyAlaLeuAspPheGluAspAlaValAlaLeuVal 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
665 CTGGTTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 714
113 aLysArgGlyAlaTyrMetGlnGluAlaAlaProAlaAspSerGlyLys 130
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
715 GATCGCGCGCAGTTCATGCAAGAGCCGTACCGGAGAGCGGCGCTA 764
130 eTValAlaValLeuAsnThrProValGluValIleGluGlnAlaCysGln 146
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
765 TGGCGGCATCATCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 814
147 LysAlaSerGlnLeuGlyValAlaThrProAlaAspTyrAsnThrProAl 163
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
815 GAACTGCAGAAAGTCAGCTGTTCTCCGGTAACCTTAACCTCCGGG 864
163 aGlnIleValIleAlaGlyGluValAlaValaAspArgAlaValGlu 180
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
865 ACAGTGTGTTATGCGCGTCATAAAGAGCGCTGACGCTGCTGCTG 914
180 euleGlnGluAlaGlyValAlaLysArgLeuIleProLeuLysValSerGly 196
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
915 CCTGTAAGCGCGCGCGCAAAACGCGCGCTGCTGCTGCTGCTGCTG 964
197 ProPheIleThrAlaLeuGlnProAlaSerGlnIleLeuAlaGlu 213
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
965 CCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1014
213 rLeuAlaGlnValSerPheSerAspPheThrCysProLeuValGlyAsn 230
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1015 ATTGACCAATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1064
230 hGlnAlaLeuAlaValMetGlnLysGlnAsp...IleAlaGlnLeuLeuThr 245

```

seq\_name: gb\_bai:ECOFABD

seq\_documentation\_block:

LOCUS ECOFABD 1608 bp DNA BCT 26-Apr-1993

DEFINITION Escherichia coli malonyl coenzyme A-acyl carrier protein (fabD)

gene, complete cds.

VERSION M87040.1 GI:145885

KEYWORDS fabD gene; malonyl coenzyme A-acyl carrier protein transacylase.

SOURCE Escherichia coli (strain K-12) DNA.

ORGANISM Escherichia coli

Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

Escherichia

1 (bases 1 to 1608)

Verwoert,I.G.S., Verdre, E.C., van der Linden, K.H., Nijkamp, H.J.

and Stuitje, A.R.

Cloning, nucleotide sequence, and expression of the Escherichia

coli fabD gene, encoding malonyl coenzyme A-acyl carrier protein

transacylase

J. Bacteriol. 174, 2851-2857 (1992)

92234941

FEATURES

source

CDs

location/Qualifiers

1..1608

/organism="Escherichia coli"

/strain="K-12"

/db\_xref="taxon:562"

<1..516

/note="ORF1"

/codon\_start=1

/transl\_table=11

/protein\_id="AAA23741.1"

/db\_xref="GI:145885"

/translation="DPTDRGTTIIIFGDGAAVLAASEPGLIITLHNDGSGYGLT

LPNADRYNPENSIHLMAGNEVEKAVTELAIHVDTELAANNLDSOLDIMYPRQNT

RISATVKKIKGMDNVVYTLDRHNTSAASVPCALDENVRGRIRKPOLVLEAFGG

GFTMGSLVRF"

521..524

/note="possible ribosome binding site for ORF2"

532..1461

/gene="fabD"

532..1461

/gene="fabD"

/codon\_start=1

/transl\_table=11

/function="fatty acid biosynthesis"

/evidence="experimental"

/product="malonyl coenzyme A-acyl carrier protein

transacylase"

/protein\_id="AAA23742.1"

/db\_xref="GI:145887"

/translation="MTRFAVFPGGSGTQVGLADMAAYPEVETFAEASAGYDL

WALTQGPALVELNKTWQTPALITASVALYRWQOGGKAPAMAGHSLGYSALVCA

GVIDEADAVLENGKFEQEAIVPGTGMAAIIIGDDASIAKCEEAEEQVSPV

FNSPGVVVAGHKEAVERAGACKAAKRRALLPVPVSPSHCALMKRPAADLAVELK